

Sun Oct 22 12:45:53 2000

us-08-894-356c-21.rpr

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GenCore version 4.5
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OW protein - protein search, using SW model

Run on: October 20, 2000, 01:34:22 ; Search time 11.52 seconds
(without alignments)
33,052 Million cell updates/sec

Title: US-08-894-356c-21

Perfect score: 40

Sequence: 1 DFGCK 6

Scoring table: BLOSUM62
Gapop 10.0, Capext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.65:
2: PIR.1:
3: PIR.3:
4: PIR.4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	40	100.0	443 2 T45574	anthranilate N-hyd
2	40	100.0	450 2 T45573	anthranilate N-hyd
3	40	100.0	451 2 T00527	hypothetical prote
4	40	100.0	455 2 T09666	probable anthranil
5	40	100.0	460 2 T03274	har201 protein, hy
6	40	100.0	461 2 T00918	hypothetical prote
7	40	100.0	475 2 T45961	anthranilate N-ben
8	36	90.0	430 2 T46216	anthranilate N-ben
9	35	87.5	442 2 T10717	anthranilate N-ben
10	35	87.5	445 2 T10717	anthranilate N-ben
11	35	87.5	445 2 T10719	anthranilate N-ben
12	35	87.5	446 2 T10711	anthranilate N-ben
13	35	87.5	485 2 T33865	hypothetical prote
14	35	87.5	572 2 T01056	hypothetical prote
15	34	85.0	113 2 S60978	wound-induced prot
16	34	85.0	129 2 S60978	probable membrane
17	34	85.0	216 2 T02913	hypothetical prote
18	34	85.0	519 2 T02913	hypothetical prote
19	34	85.0	667 2 S54300	transketolase (EC
20	34	85.0	667 2 T69723	transketolase (EC
21	33	82.5	730 2 T47886	hypothetical prote
22	33	80.0	234 2 A15486	response regulator
23	32	80.0	299 2 T36369	hypothetical prote
24	32	80.0	346 2 T10173	24-sterol C-methyl
25	32	80.0	367 2 T06780	probable 24-sterol
26	32	80.0	409 2 T19688	hypothetical prote
27	32	80.0	428 2 T48008	hypothetical prote
28	31	77.5	106 2 B64350	hypothetical prote
29	31	77.5	110 1 F71129	hypothetical prote

30	31	77.5	110 2 F75034	hypothetical prote
31	31	77.5	112 2 J00131	biophenyl-2,3-diol
32	31	77.5	158 2 S35201	serine proteinase
33	31	77.5	215 2 G70342	hypothetical prote
34	31	77.5	261 2 S74761	hypothetical prote
35	31	77.5	291 1 B53419	biophenyl-2,3-diol
36	31	77.5	293 1 DAPSPC	biophenyl-2,3-diol
37	31	77.5	296 2 J00103	azarene castazole
38	31	77.5	299 2 A57264	biophenyl-2,3-diol
39	31	77.5	299 2 A28718	2,3-dihydroxybiphe
40	31	77.5	299 2 T31282	sugar-phosphate de
41	31	77.5	316 2 T69978	hypothetical prote
42	31	77.5	335 2 T48319	alcohol dehydrogen
43	31	77.5	371 2 B69502	urophosphoryl-II C
44	31	77.5	393 2 S02185	mannose-6-phosphat
45	31	77.5	412 2 T60135	

ALIGNMENTS

RESULT 1
T45574
anthranilate N-hydroxycinnamoyl/phenyltransferase-like protein - Arabidopsis thalian
N/Alternate names: protein P11C1.120
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
R/Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Maves, H.W.;
submitted to the Protein Sequence Database, December 1999
A/Reference number: 233007
A/Accession: T45574
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-443 <BAR>
A/Cross-references: EMBL:AL132976
A/Experimental source: cultivar Columbia; BAC clone P11C1
C/Genetics:
A/Map position: 3
A/Note: P11C1.120

Query Match
Best Local Similarity 100.0%: Score 40; DB 2; Length 443;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 DFGCK 6
DB 386 DFGCK 391

RESULT 2

T45573
anthranilate N-hydroxycinnamoyl/phenyltransferase-like protein - Arabidopsis thalian
N/Alternate names: protein P11C1.110
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
R/Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Maves, H.W.;
submitted to the Protein Sequence Database, December 1999
A/Reference number: 233007
A/Accession: T45573
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-450 <BAR>
A/Cross-references: EMBL:AL132976
A/Experimental source: cultivar Columbia; BAC clone P11C1
C/Genetics:
A/Map position: 3
A/Note: P11C1.110

Query Match 100.0%: Score 40; DB 2; Length 450;

Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 391 DRGWCK 396

RESULT 3

T00527
Hypothetical protein T20K24.8 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Apr-1999

C:Accession: T00527

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1997

A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.

A:Reference number: 214167

A:Accession: T00527

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-451 <R0U>

A:Cross-references: EMBL:AC003393; NID:93176701; PID:93176709

A:Experimental source: cultivar Columbia

C:Genetics:

A:Map position: 2

A:Introns: 322/1

A>Note: T20K24.8

Query Match
Best Local Similarity 100.0%; Score 40; DB 2; Length 451;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 397 DRGWCK 402

RESULT 4

T09666

Probable anthranilate N-benzoyltransferase (EC 2.3.1.144) - muskmelon (fragment)

N:Alternate names: anthranilate N-hydroxycinnamoyl/benzoyltransferase

C:Species: Cucumis melo (muskmelon)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C:Accession: T09666

R:Aggelis, A.; John, I.; Karvouni, Z.; Grierson, D.

Plant Mol. Biol. 33, 313-322, 1997

A:Title: Characterization of two cDNA clones for mRNAs expressed during ripening of melo

A:Reference number: 216810; MID:97188564

A:Accession: T09666

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-455 <RAG>

A:Cross-references: EMBL:Z70521; NID:6991794; PID:6234032

A:Experimental source: cultivar Cantaloupe charantais; pericarp of ripe fruit

C:Keywords: acyltransferase; coenzyme A

Query Match
Best Local Similarity 100.0%; Score 40; DB 2; Length 455;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 374 DRGWCK 379

RESULT 5

T03274

har201 protein, hypersensitivity-related - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 07-May-1999

C:Accession: T03274

R:Czernek, P.; Huang, H.C.; Marco, Y.

Plant Mol. Biol. 31, 255-265, 1996

A:Title: Characterization of har201 and har515, two tobacco genes preferentially expr

A:Reference number: 214876; MID:9633929

A:Accession: T03274

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-460 <CZ2>

A:Cross-references: EMBL:X05343; NID:91171576; PID:6220213

A:Experimental source: cultivar bottom special

C:Genetics:

A:Gene: har201

Query Match
Best Local Similarity 100.0%; Score 40; DB 2; Length 460;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 382 DRGWCK 387

RESULT 6

T00918

hypothetical protein F21B7.32 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999

C:Accession: T00918

R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.;

et al.; A.; Ecker, J.R.

submitted to the EMBL Data Library, January 1998

A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.

A:Reference number: 214208

A:Accession: T00918

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-461 <SHI>

A:Cross-references: EMBL:AC002560; NID:92618677; PID:92809263; GSPDB:GN00059; ATSP:F2

C:Genetics:

A:Gene: ATSP:F21B7.32

A:Map position: 1

Query Match
Best Local Similarity 100.0%; Score 40; DB 2; Length 461;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRGWCK 6
DB 400 DRGWCK 405

RESULT 7

T45961

anthranilate N-benzoyltransferase-like protein - Arabidopsis thaliana

N:Alternate names: protein F7J8.190

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T45961

R:Beran, M.; Zimmermann, W.; Gruenleisen, A.; Wambutt, R.; Bancroft, I.; Wees, H.W.;

submitted to the Protein Sequence Database, January 2000

A:Reference number: 223018

A:Accession: T45961

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-475 <BEV>

A:Cross-references: EMBL:AL137189

A:Experimental source: cultivar Columbia; BAC clone F7J8

C:Genetics:

A:Map position: 5

A>Note: F7J8.190

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XX      MO9625500-A1.
PM      22-AUG-1996.
XX
XX      16-FEB-1996; 96MO-JP00348.
XX
XX      30-JAN-1996; 96JP-0046534.
PR      17-FEB-1995; 95JP-0067159.
PR      29-JUN-1995; 95JP-0196915.
XX
XX      (SUNR ) SUNTORI LTD.
XX
XX      Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
PI      Nakao M, Tanaka Y, Yonekura K;
DR      MPI: 1996-393401/39.
DR      N-PSDB: W04724.
XX
XX      DNA coding for aromatic acyl transferase - for transforming plants
PT      which produce anthocyanin pigments and thus altering colour tone,
XX      e.g. of flowers
XX
XX      Claim 4; Page 61-65; 94pp: Japanese.
XX
XX      Vectors containing DNA fragments encoding proteins of plant origin
CC      with aromatic acyl transferase activity may be used to transform
CC      plants which produce anthocyanin pigments. The aromatic acyl
CC      transferase acylates the pigments in the flower resulting in colour
CC      tone changes and allowing new colourations to be produced. Six
CC      specific DNA sequences encoding aromatic acyl transferase from
CC      different plants are described in T37308-T37313.
XX
XX      Sequence 448 AA;
SQ

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Query Match 100.0%; Score 40; DB 17; Length 448;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DRGNR 6
DB      390 dfgw9k 395

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RESULT 7
 ID W04727 standard: Protein; 450 AA.
 AC W04727;
 XX
 XX 06-FEB-1997 (first entry)
 DE Aromatic acyl transferase of Lavandula angustifolia.
 XX
 XX Aromatic acyl transferase; transformation; anthocyanin pigment;
 KW plants; acylation; colour; tone; colouration; colour change;
 KW Gentiana triflora; Petunia hybrida; Perilla ocimoides;
 KW Senecio cruentus; Lavandula angustifolia.
 XX
 OS Lavandula angustifolia (clone plant1).
 XX
 XX Key Location/Qualifiers
 XX Misc-difference 1 /note- "Unidentified amino acid"
 XX
 XX W09625500-A1.
 XX
 XX 22-AUG-1996.
 XX
 XX 16-FEB-1996; 96MO-JP00348.
 XX
 XX 30-JAN-1996; 96JP-0046534.
 XX

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PR      17-FEB-1995; 95JP-0067159.
PR      29-JUN-1995; 95JP-0196915.
XX
XX      (SUNR ) SUNTORI LTD.
XX
XX      Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
PI      Nakao M, Tanaka Y, Yonekura K;
DR      MPI: 1996-393401/39.
XX
XX      DNA coding for aromatic acyl transferase - for transforming plants
PT      which produce anthocyanin pigments and thus altering colour tone,
XX      e.g. of flowers
XX
XX      Claim 4; Page 73-76; 94pp: Japanese.
XX
XX      Vectors containing DNA fragments encoding proteins of plant origin
CC      with aromatic acyl transferase activity may be used to transform
CC      plants which produce anthocyanin pigments. The aromatic acyl
CC      transferase acylates the pigments in the flower resulting in colour
CC      tone changes and allowing new colourations to be produced. Six
CC      specific DNA sequences encoding aromatic acyl transferase from
CC      different plants are described in T37308-T37313. NOTE: This
CC      sequence is supposed to cross reference with the nucleotide
CC      described in T37313, however there are so many discrepancies between
CC      the polypeptide decoded from that sequence and this polypeptide
CC      given in the specification that the indexer decided not to cross
XX      reference the two.
XX
XX      Sequence 450 AA;
SQ

```

Query Match 100.0%; Score 40; DB 17; Length 450;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 DRGNR 6
DB      393 dfgw9k 398

```

RESULT 8
 ID W04726 standard: Protein; 454 AA.
 AC W04726;
 XX
 XX 06-FEB-1997 (first entry)
 DE Aromatic acyl transferase of Senecio cruentus.
 XX
 XX Aromatic acyl transferase; transformation; anthocyanin pigment;
 KW plants; acylation; colour; tone; colouration; colour change;
 KW Gentiana triflora; Petunia hybrida; Perilla ocimoides;
 KW Senecio cruentus; Lavandula angustifolia.
 XX
 OS Senecio cruentus (clone pc8r8).
 XX
 XX W09625500-A1.
 XX
 XX 22-AUG-1996.
 XX
 XX 16-FEB-1996; 96MO-JP00348.
 XX
 XX 30-JAN-1996; 96JP-0046534.
 PR 17-FEB-1995; 95JP-0067159.
 PR 29-JUN-1995; 95JP-0196915.
 XX
 XX (SUNR) SUNTORI LTD.
 XX
 XX Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
 PI Nakao M, Tanaka Y, Yonekura K;
 XX